

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,759

DATE: 12/14/2001

TIME: 09:52:58

Input Set : A:\2739.2001-001 seq.txt

Output Set: N:\CRF3\12142001\I003759.raw

ENTERED

#2

3 <110> APPLICANT: Wicher, Kryzysztow B.
4 Holst, Olof Peder
5 Hachem, Maher Youssef Abou
6 Karlsson, Eva Margareta Nordberg
7 Hreggvidsson, Gudmundur O.
9 <120> TITLE OF INVENTION: Thermostable Cellulase
11 <130> FILE REFERENCE: P5099PC00
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/003,759
C--> 13 <141> CURRENT FILING DATE: 2001-10-23
13 <150> PRIOR APPLICATION NUMBER: PCT/IS01/00012
14 <151> PRIOR FILING DATE: 2001-06-15
16 <150> PRIOR APPLICATION NUMBER: 09/594,884
17 <151> PRIOR FILING DATE: 2000-06-15
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1877
25 <212> TYPE: DNA
26 <213> ORGANISM: Rhodothermus marinus
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (710)..(1495)
31 <223> OTHER INFORMATION:
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36 tgcgtgcgca cgcactgggc gctgggcgag tttcccttct acttgcgtcca gattgccct 120
38 tacgactacg ggccgaacgc ccgcaacgcag cgtgtccggg aagcgcagtt gcgcaccatg 180
40 tgcgcgtgcc tcatacgggt atggctgtga ccaccgatgt gggcgacgac cacaacacta 240
42 cctccggcgc gacaacgtga agtggcgagc gcctggcctc tgggcgctgg ccaacgacta 300
44 cggttccgg gatgtggtct actccggtcc catctacgaa cgcattggaac gtgaggatgg 360
46 ccgcctgcgg ctctatttcc gctatgccga agggggactg gtccctgcgc ccgccgacgg 420
48 cggcgcgag ttctgtgattg cgggaccgga ccgtgtcttc caccggcgcc gggtagcggg 480
50 cgaaggcgaa acgctgggtg tgtggagtcc gcgcgtctcc gatccgcagg cggtagccta 540
52 tggctgttcc aatacgcgc acgccacgct gttcaaccgg gccggcctgc ccgcttcgcc 600
54 cttccgcacc gacgactggc cggaaggcga ctgagcgacg caaccggtgc ttgcatgcca 660
56 caggggcact tcgtaccttg aagtgcctt tgtcatttca atggaataa atg aac gtc 718
57 Met Asn Val
58 1
60 atg cgt gcg gta ctg gtc ctg agc ctg tta ttg ctg ttt gga tgc gac 766
61 Met Arg Ala Val Leu Val Leu Ser Leu Leu Leu Phe Gly Cys Asp
62 5 10 15
64 tgg ctc ttt ccc gat ggc gac aac gga aag gaa ccg gag cct gag ccc 814
65 Trp Leu Phe Pro Asp Gly Asp Asn Gly Lys Glu Pro Glu Pro Glu Pro
66 20 25 30 35
68 gag ccg acc gtc gag ctg tgc gga cgc tgg gac gcg cgc gat gtg gcc 862
69 Glu Pro Thr Val Glu Leu Cys Gly Arg Trp Asp Ala Arg Asp Val Ala
70 40 45 50

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72 ggg ggg cgc tac cgg gtg atc aac aac gta tgg ggc gcg gag acc gcc      910
73 Gly Gly Arg Tyr Arg Val Ile Asn Asn Val Trp Gly Ala Glu Thr Ala
74          55          60          65
76 cag tgc att gag gtc gga ctg gaa acg ggc aac ttc acg atc aca cgg      958
77 Gln Cys Ile Glu Val Gly Leu Glu Thr Gly Asn Phe Thr Ile Thr Arg
78          70          75          80
80 gcc gat cac gac aac ggc aac aac gtg gcc gcc tat ccg gcc atc tac      1006
81 Ala Asp His Asp Asn Gly Asn Asn Val Ala Ala Tyr Pro Ala Ile Tyr
82          85          90          95
84 ttc ggg tgc cac tgg ggc gcc tgc acg agc aat tcg gga ttg ccg cgg      1054
85 Phe Gly Cys His Trp Gly Ala Cys Thr Ser Asn Ser Gly Leu Pro Arg
86 100          105          110          115
88 cgc gtg cag gag ctg tcc gac gtg cgc acg agc tgg acg ctc acg ccg      1102
89 Arg Val Gln Glu Leu Ser Asp Val Arg Thr Ser Trp Thr Leu Thr Pro
90          120          125          130
92 atc acg acg ggc cgc tgg aat gcc gcc tac gac atc tgg ttc agt ccc      1150
93 Ile Thr Thr Gly Arg Trp Asn Ala Ala Tyr Asp Ile Trp Phe Ser Pro
94          135          140          145
96 gtc acg aat tcc ggc aac ggc tac agc ggc ggc gcc gag ctg atg atc      1198
97 Val Thr Asn Ser Gly Asn Gly Tyr Ser Gly Gly Ala Glu Leu Met Ile
98          150          155          160
100 tgg ctg aac tgg aac ggc ggc gtg atg ccg ggc ggc agc cgc gtg gcc      1246
101 Trp Leu Asn Trp Asn Gly Gly Val Met Pro Gly Gly Ser Arg Val Ala
102          165          170          175
104 acc gtg gaa ctg gcc ggg gcc acc tgg gaa gtc tgg tat gcc gac tgg      1294
105 Thr Val Glu Leu Ala Gly Ala Thr Trp Glu Val Trp Tyr Ala Asp Trp
106 180          185          190          195
108 gac tgg aat tac atc gcc tac cgg cgc acg acg ccc acc acg tcg gtg      1342
109 Asp Trp Asn Tyr Ile Ala Tyr Arg Arg Thr Thr Pro Thr Thr Ser Val
110          200          205          210
112 agc gag ctg gac ctg aag gcc ttc atc gac gac gcg gtc gcc cgc ggc      1390
113 Ser Glu Leu Asp Leu Lys Ala Phe Ile Asp Asp Ala Val Ala Arg Gly
114          215          220          225
116 tac atc cgg ccg gag tgg tat ctg cat gcg gtg gag acg ggc ttc gaa      1438
117 Tyr Ile Arg Pro Glu Trp Tyr Leu His Ala Val Glu Thr Gly Phe Glu
118          230          235          240
120 ctc tgg gag ggc ggg gcc ggt ctg cga agc gcc gat ttt tcc gta acg      1486
121 Leu Trp Glu Gly Gly Ala Gly Leu Arg Ser Ala Asp Phe Ser Val Thr
122          245          250          255
124 gtg cag tag cctgtcacac gggcaccagc gtaggccaga gaagcaccgc      1535
125 Val Gln
126 260
128 tcggggcgct tatgcgggcg gccgtcgctt tgtgcctgac tttgtagtgc gctacggagg      1595
130 cgtcagcccg cgtggtgcgt ttccctggag gcgcttcgtt tcgtgccgga cgagaactta      1655
132 tccgaaaagc aagggagaga cctggtaagc cagggctttg cactgcgcac cagaagcacg      1715
134 ggtttgtagt aagccacgaa ggcgtccgcc gaagtggcct caccgcgcac ggcacttcgc      1775
136 tgcgtccgt gctgactac gagcgcgtt gccgtgcttc aaacggcagg ctataaagct      1835
138 atacaggtcg aaatcgcgaa cttctccgac acttacaac ac      1877
141 <210> SEQ ID NO: 2

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142 <211> LENGTH: 261
143 <212> TYPE: PRT
144 <213> ORGANISM: Rhodothermus marinus
146 <400> SEQUENCE: 2
148 Met Asn Val Met Arg Ala Val Leu Val Leu Ser Leu Leu Leu Phe
149 1 5 10 15
152 Gly Cys Asp Trp Leu Phe Pro Asp Gly Asp Asn Gly Lys Glu Pro Glu
153 20 25 30
156 Pro Glu Pro Glu Pro Thr Val Glu Leu Cys Gly Arg Trp Asp Ala Arg
157 35 40 45
160 Asp Val Ala Gly Gly Arg Tyr Arg Val Ile Asn Asn Val Trp Gly Ala
161 50 55 60
164 Glu Thr Ala Gln Cys Ile Glu Val Gly Leu Glu Thr Gly Asn Phe Thr
165 65 70 75 80
168 Ile Thr Arg Ala Asp His Asp Asn Gly Asn Asn Val Ala Ala Tyr Pro
169 85 90 95
172 Ala Ile Tyr Phe Gly Cys His Trp Gly Ala Cys Thr Ser Asn Ser Gly
173 100 105 110
176 Leu Pro Arg Arg Val Gln Glu Leu Ser Asp Val Arg Thr Ser Trp Thr
177 115 120 125
180 Leu Thr Pro Ile Thr Thr Gly Arg Trp Asn Ala Ala Tyr Asp Ile Trp
181 130 135 140
184 Phe Ser Pro Val Thr Asn Ser Gly Asn Gly Tyr Ser Gly Gly Ala Glu
185 145 150 155 160
188 Leu Met Ile Trp Leu Asn Trp Asn Gly Gly Val Met Pro Gly Gly Ser
189 165 170 175
192 Arg Val Ala Thr Val Glu Leu Ala Gly Ala Thr Trp Glu Val Trp Tyr
193 180 185 190
196 Ala Asp Trp Asp Trp Asn Tyr Ile Ala Tyr Arg Arg Thr Thr Pro Thr
197 195 200 205
200 Thr Ser Val Ser Glu Leu Asp Leu Lys Ala Phe Ile Asp Asp Ala Val
201 210 215 220
204 Ala Arg Gly Tyr Ile Arg Pro Glu Trp Tyr Leu His Ala Val Glu Thr
205 225 230 235 240
208 Gly Phe Glu Leu Trp Glu Gly Gly Ala Gly Leu Arg Ser Ala Asp Phe
209 245 250 255
212 Ser Val Thr Val Gln
213 260
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 786
218 <212> TYPE: DNA
219 <213> ORGANISM: Rhodothermus marinus
221 <400> SEQUENCE: 3
222 atgaacgtca tgcgtgcggt actggctctg agcctgttat tgctgttttg atgcgactgg 60
224 ctcttttccc atggcgacaa cggaaaggaa ccggagcctg agcccgagcc gaccgtcgag 120
226 ctgtgcggac gctgggacgc gcgcgatgtg gccggggggc gctaccgggt gatcaacaac 180
228 gtatggggcg cggagaccgc ccagtgcatt gaggtcggac tggaaacggg caacttcacg 240
230 atcacacggg ccgatcacga caacggcaac aacgtggccg cctatccggc catctacttc 300
232 ggggtgccact ggggcgccctg cacgagcaat tcgggattgc cgcggcgcgt gcaggagctg 360

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234 tccgacgtgc gcacgagctg gacgctcacg cccgacacga cgggcccgtg gaatgccgcc      420
236 tacgacatct ggttcagtcg cgtcacgaat tccggcaacg gctacagcgg cggcgccgag      480
238 ctgatgatct ggctgaactg gaacggcgccg gtgatgccgg gcggcagccg cgtggccacc      540
240 gtggaactgg ccggggccac ctgggaagtc tggatgccgg actgggactg gaattacatc      600
242 gcctaccggc gcacgacgcc caccacgtcg gtgagcgagc tggacctgaa ggccttcac      660
244 gacgacgcgg tcgcccgcgg ctacatccgg ccggagtggg atctgcatgc ggtggagacg      720
246 ggcttcgaac tctgggaggg cggggccggg ctgcgaagcg ccgatttttc cgtaacgggtg      780
248 cagtag
251 <210> SEQ ID NO: 4
252 <211> LENGTH: 1134
253 <212> TYPE: DNA
254 <213> ORGANISM: Pyrococcus furiosus
256 <220> FEATURE:
257 <221> NAME/KEY: exon
258 <222> LOCATION: (82)..(1041)
259 <223> OTHER INFORMATION:
261 <400> SEQUENCE: 4
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264 aacaaatttg gaggatgtcc a atg agc aag aaa aag ttc gtc atc gta tct      111
265                               Met Ser Lys Lys Lys Phe Val Ile Val Ser
266                               1           5           10
268 atc tta aca atc ctt tta gta cag gca ata tat ttt gta gaa aag tat      159
269 Ile Leu Thr Ile Leu Leu Val Gln Ala Ile Tyr Phe Val Glu Lys Tyr
270                               15           20           25
272 cat acc tct gag gac aag tca act tca aat acc tca tct aca cca ccc      207
273 His Thr Ser Glu Asp Lys Ser Thr Ser Asn Thr Ser Ser Thr Pro Pro
274                               30           35           40
276 caa aca aca ctt tcc act acc aag gtt ctc aag att aga tac cct gat      255
277 Gln Thr Thr Leu Ser Thr Thr Lys Val Leu Lys Ile Arg Tyr Pro Asp
278                               45           50           55
280 gac ggt gag tgg cca gga gct cct att gat aag gat ggt gat ggg aac      303
281 Asp Gly Glu Trp Pro Gly Ala Pro Ile Asp Lys Asp Gly Asp Gly Asn
282                               60           65           70
284 cca gaa ttc tac att gaa ata aac cta tgg aac att ctt aat gct act      351
285 Pro Glu Phe Tyr Ile Glu Ile Asn Leu Trp Asn Ile Leu Asn Ala Thr
286 75                               80           85           90
288 gga ttt gct gag atg acg tac aat tta acc agc ggc gtc ctt cac tac      399
289 Gly Phe Ala Glu Met Thr Tyr Asn Leu Thr Ser Gly Val Leu His Tyr
290                               95          100          105
292 gtc caa caa ctt gac aac att gtc ttg agg gat aga agt aat tgg gtg      447
293 Val Gln Gln Leu Asp Asn Ile Val Leu Arg Asp Arg Ser Asn Trp Val
294                               110         115         120
296 cat gga tac ccc gaa ata ttc tat gga aac aag cca tgg aat gca aac      495
297 His Gly Tyr Pro Glu Ile Phe Tyr Gly Asn Lys Pro Trp Asn Ala Asn
298                               125         130         135
300 tac gca act gat ggc cca ata cca tta ccc agt aaa gtt tca aac cta      543
301 Tyr Ala Thr Asp Gly Pro Ile Pro Leu Pro Ser Lys Val Ser Asn Leu
302                               140         145         150
304 aca gac ttc tat cta aca atc tcc tat aaa ctt gag ccc aag aac gga      591

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305 Thr Asp Phe Tyr Leu Thr Ile Ser Tyr Lys Leu Glu Pro Lys Asn Gly
306 155                               160                               165                               170
308 ctg cca att aac ttc gca ata gaa tcc tgg tta acg aga gaa gct tgg      639
309 Leu Pro Ile Asn Phe Ala Ile Glu Ser Trp Leu Thr Arg Glu Ala Trp
310                               175                               180                               185
312 aga aca aca gga att aac agc gat gag caa gaa gta atg ata tgg att      687
313 Arg Thr Thr Gly Ile Asn Ser Asp Glu Gln Glu Val Met Ile Trp Ile
314                               190                               195                               200
316 tac tat gac gga tta caa ccg gct ggc tcc aaa gtt aag gag att gta      735
317 Tyr Tyr Asp Gly Leu Gln Pro Ala Gly Ser Lys Val Lys Glu Ile Val
318                               205                               210                               215
320 gtc cca ata ata gtt aac gga aca cca gta aat gct aca ttt gaa gta      783
321 Val Pro Ile Ile Val Asn Gly Thr Pro Val Asn Ala Thr Phe Glu Val
322                               220                               225                               230
324 tgg aag gca aac att ggt tgg gag tat gtt gca ttt aga ata aag acc      831
325 Trp Lys Ala Asn Ile Gly Trp Glu Tyr Val Ala Phe Arg Ile Lys Thr
326 235                               240                               245                               250
328 cca atc aaa gag gga aca gtg aca att cca tac gga gca ttt ata agt      879
329 Pro Ile Lys Glu Gly Thr Val Thr Ile Pro Tyr Gly Ala Phe Ile Ser
330                               255                               260                               265
332 gtt gca gcc aac att tca agc tta cca aat tac aca gaa ctt tac tta      927
333 Val Ala Ala Asn Ile Ser Ser Leu Pro Asn Tyr Thr Glu Leu Tyr Leu
334                               270                               275                               280
336 gag gac gtg gag att gga act gag ttt gga acg cca agc act acc tcc      975
337 Glu Asp Val Glu Ile Gly Thr Glu Phe Gly Thr Pro Ser Thr Thr Ser
338                               285                               290                               295
340 gcc cac cta gag tgg tgg atc aca aac ata aca cta act cct cta gat      1023
341 Ala His Leu Glu Trp Trp Ile Thr Asn Ile Thr Leu Thr Pro Leu Asp
342                               300                               305                               310
344 aga cct ctt att tcc taa atttcggcaa cctgggaatt atcaagttta      1071
345 Arg Pro Leu Ile Ser
346 315
348 agaaaagggtg gagttgctaa agaattcaaa gaaaatttga aaagtaactt ttattgtgat      1131
350 ctc                               1134
353 <210> SEQ ID NO: 5
354 <211> LENGTH: 319
355 <212> TYPE: PRT
356 <213> ORGANISM: Pyrococcus furiosus
358 <220> FEATURE:
359 <221> NAME/KEY: SIGNAL
360 <222> LOCATION: (1)..(19)
361 <223> OTHER INFORMATION:
363 <220> FEATURE:
364 <221> NAME/KEY: DOMAIN
365 <222> LOCATION: (28)..(49)
366 <223> OTHER INFORMATION: Linker Moiety
368 <220> FEATURE:
369 <221> NAME/KEY: DOMAIN
370 <222> LOCATION: (50)..(319)

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/003,759

DATE: 12/14/2001

TIME: 09:52:59

Input Set : A:\2739.2001-001 seq.txt

Output Set: N:\CRF3\12142001\I003759.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date